

RESULT 2
 ABK92167
 ID ABK92167 standard; DNA; 3810 BP.
 XX
 AC ABK92167;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE
 XX
 KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
 KW gene therapy; gene; ds.
 XX
 OS Mammalia.
 XX
 PN WO2002032045-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US032045.
 XX
 PR 13-OCT-2000; 2000US-00687576.
 PR 08-DEC-2000; 2000US-00733288.
 PR 08-DEC-2000; 2000US-00733742.
 PR 24-JAN-2001; 2001US-0263957P.
 PR 16-MAR-2001; 2001US-0276791P.
 PR 16-MAR-2001; 2001US-0276886P.
 PR 06-APR-2001; 2001US-0281922P.
 PR 24-APR-2001; 2001US-0286214P.
 PR 30-APR-2001; 2001US-00847046.
 PR 04-MAY-2001; 2001US-0288589P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 XX
 DR WPI; 2002-471335/50.
 DR P-PSDB; ABMG61852.
 XX
 PT Detecting a prostate cancer-associated transcript in a cell in a patient,
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
 PT by determining if prostate cancer-associated genes are expressed in a
 PT prostate tissue.
 XX
 PS Claim 22; Page 339-340; 436pp; English.
 XX
 CC The present invention relates to methods of detecting a prostate cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with prostate cancer-
 CC associated polynucleotides (designated PC genes) that selectively
 CC hybridize to a sequence that is at least 80% identical to them. The
 CC prostate cancer-associated polynucleotide sequences are differentially
 CC expressed in prostate tumour tissue or in prostate cancer and are derived
 CC from the tissues of various organisms such as humans or other mammals
 CC (e.g., mice, sheep and dogs). The methods of the invention are useful for
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
 CC associated genes are useful for diagnosing or treating prostate cancer,
 CC as well as for identifying modulators of prostate cancer or agents that
 CC inhibit prostate cancer. The nucleic acid sequences are particularly
 CC useful in gene therapy, as a vaccine or in antisense applications.
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
 CC sequences
 XX
 SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0 Length: 3810
 Score: 1123.00 Matches: 1123
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 99.6% Indels: 0
 DB: 6 Gaps: 0

US-10-643-795A-123 (1-1127) × ABK92167 (1-3810)

Qy 5 ThrGluLysProThrAspAlaTyrGlyGluLeuAspPheThrGlyAlaGlyArgLysHis 24

Db 3 ACGGAGAAACCCACCGATGCCATCAGGAGACTGGACTTCACGGGGCGCGCCGCAAGAAC 62
Qy 25 SerAsnPheLeuArgIleSerAspArgThrAspPheProAlaAlaValTyrSerLeuValThr 44
Db 63 AGGAAATTCCCCTCGGCCTCTGACCCGAACGGATCCAGCTCAGTTATAGTCCTGGTCACA 122
Qy 45 ArgThrTrpGlyPheArgAlaProAsnLeuValValSerValLeuGlyGlySerGlyGly 64
Db 123 CGAACATGGGGCTTCGGTGCCCCGAACTGGTGGTGTCAAGTGTCTGGGGGATCGGGGGC 182
Qy 65 ProValLeuGlnThrTrpLeuGlnAspLeuLeuArgArgGlyLeuValArgAlaAlaGln 84
Db 183 CCGCTCTCGAACCTGCGTCAGGACCTGCTGGCTGGCTGGCTGGGGCTGGCCAG 242
Qy 85 SerThrGlyAlaTrpIleValThrGlyGlyLeuHisThrGlyIleGlyArgHisValGly 104
Db 243 AGGACAGGAGGACTTGATGTCACTGGGGCTCAGCACACGGGACATGGGGGGCATGGTGT 302
Qy 105 ValAlaValArgAspHisGlnMetAlaSerThrGlyGlyThrLysValValAlaMetGly 124
Db 303 GTGGCTGTACGSGAACATCAGATGGGCAAGCACTGGGGGACCAAGTGGTGGCCATGGGT 362
Qy 125 ValAlaProTrpGlyValValArgAsnArgAspThrLeuIleAsnProIysGlySerPhe 144
Db 363 GTGGCCCCCTGGGGTGTGGTCCGGNATAGGACACCCCTCATCAAACCCCAAGGGCTGGTC 422
Qy 145 ProAlaArgItyArgTrpArgGlyAspProGluAspGlyValGlnPheProLeuAspItyr 164
Db 423 CCTGGGGGGTACGGTGGCGGGTGGACCAGGACACTGGGGGACAGTTTCCCCTGGACTAC 482
Qy 165 AsnTyrSerAlaPhePheLeuValAspAspGlyThrHisGlyCysLeuGlyGlyGluAsn 184
Db 483 AACTACTCGGCTCTCTCTCTGGTGGACGACGGCACACGGCTGGCTGGGGGGCAGAAC 542
Qy 185 ArgPheArgLeuArgLeuGluSerTyrIleSerGlnGlnLysThrGlyValGlyGlyThr 204
Db 543 CGCTTCCGGCTTGSGGCTGGAGCTCTACATCTCACAGCAGAAGACGGGGCTGGGGGGACT 602
Qy 205 GlyIleAspIleProValIleLeuLeuIleAspGlyAspGluLysMetLeuThrArg 224
Db 603 GGAATTCGACATCCCTGTCCTGCTCCCTCTGGATGATGGTGTAGGAAAGATGTTGACGGGA 662
Qy 225 IleGluAsnAlaThrGlnAlaGlnLeuProCysLeuLeuValAlaGlySerGlyGlyAla 244
Db 663 ATAGAGAAACCCACCCAGGCTCAGCTCCATGTCCTCTGGCTGGCTGGGGAGCT 722
Qy 245 AlaAspCysIleAlaGluThrLeuIleAspGlyAspThrLeuAlaProGlySerGlyGlyAlaArg 264
Db 723 GCCTGGACTGCTCTGGGAGACCCCTGGAAAGACACTCTGGCCCCAAGGGAGTGGGGGAGCCGG 782
Qy 265 GlnGlyGluAlaArgAspArgIleArgArgPhePheProLysGlyAspLeuGluValLeu 284
Db 783 CAAGGCCGAAGCCGAGATCGGAATCAGGCGTTCTCCAAAGGGGACCTTGAGGTCTG 842
Qy 285 GlnAlaGlnValGluArgIleMetThrArgLysGluLeuLeuThrValTyrSerSerGlu 304
Db 843 CAGGCCAGGGTGGAGGAGTTATGACCCGGAAAGAGCTCCCTGACAGTCTATTCTCTGAG 902
Qy 305 AspGlySerGluGluPheGluThrIleValLeuLysAlaLeuValLysAlaCysGlySer 324
Db 903 GATGGGTCTGAGGAATTCTGGAGACCATAGTTTGAAAGGCCCTGTAAGGCCCTGGGGAGC 962
Qy 325 SerGluAlaSerAlaTyrLeuAspGluLeuArgLeuAlaValAlaTrpAsnArgValAsp 344
Db 963 TCGGAGGCCCTCGSCTAACCTGGATGAGCTGGCTTGGCTGTGGCTGGACACGGGCTGGAC 1022
Qy 345 IleAlaGlnSerGluLeuPheArgGlyAspIleGlnTrpArgSerPheHisLeuGluAla 364
Db 1023 ATTGCCCAAGGATGAACTCTTCGGGGGACATCCAATGGGGCTCTCCATCTCGAAGACT 1082
Qy 365 SerLeuMetAspAlaLeuLeuAsnAspArgProGluPheValArgLeuLeuIleSerHis 384
Db 1083 TCCCTCATGGAGCGGCTGCTGAAATGACGGGCTCTGAGTTCTGGCTGGCTGGCTCAATTCCCAC 1142
Qy 385 GlyLeuSerLeuGlyHisPheLeuThrProMetArgLeuAlaGlnLeuTyrSerAlaAla 404

Db 1143 ||||||TCAGCCTGGCCACCTTCTGAGCCCGATGGCGCTGGGCCAACCTCTACAGGGCGGGCG 1202
 Qy 405 ProSerAsnLeuIleLeuArgAsnLeuLeuAspPheAlaSerHisSerAlaGlyThrIle 424
 Db 1203 CCCTCCAACCTCCTCATCCGAAACCTTTGGACCAAGCGTCCCACAGCAGCAGCACCMAA 1262
 Qy 425 AlaProAlaIleLeuIysGlyGlyAlaAlaGluLeuArgProProAspValIlyHisValLeu 444
 Db 1263 GCGCCGAACCCCTAAAAGGCGGAACCTCGCGAGCTCCGGCCCCCTGAGCTGGGCCATGCGTG 1322
 Qy 445 ArgMetLeuLeuGlyLysMetCysAlaProArgIyrProSerGlyGlyAlaTrpAspPro 464
 Db 1323 AGGATGCTGCTGGAGAGTAGTGTGCGCCCGAGGTACCCCTCGGGGGCCCTGGGACCCCT 1382
 Qy 465 HisProGlyGlnGlyPheGlyGluSerMetTyrIleLeuSerAspIysAlaThrSerPro 484
 Db 1383 CACCCAGGCCAACGGCTTCGCGGAGAGCACTGTAICCTGCTCGAGCAAAGGCCAACCTCGCCG 1442
 Qy 485 LeuSerLeuAspAlaGlyLeuGlyGinAlaProTrpSerAspLeuLeuLeuTrpAlaLeu 504
 Db 1443 CTCTCGCTGGATGCTGGCTCGGGAGGCCCCCTGGAGCGACCTGCTCTTGGGACTG 1502
 Qy 505 LeuLeuAsnArgAlaGlnMetAlaMetTyrPheTrpGluMetGlySerAsnAlaValSer 524
 Db 1503 TTCTGAGAACAGGGGACAGATGGCGCATGTACTTCCTGGAGATGGGTTCATAATGCAGTTCC 1562
 Qy 525 SerAlaLeuGlyAlaCysLeuLeuLeuArgValMetAlaArgLeuGluProAspAlaGlu 544
 Db 1563 TCAGCTCTTGAGGCGCTGTGGCTGCTGCCGGTATGGCACGCCCTGGAGCTGACGCTGAG 1622
 Qy 545 GluAlaLeuArgArgIysAspLeuAlaPheLysPheGluGlyMetGlyValAspLeuPhe 564
 Db 1623 GAAGCAACGCGAAGGAAGACCTGGCGCTTCAGGTTGAGGGGATGGCGCTTGGACCTCTT 1682
 Qy 565 GlyGluCysTyrArgSerSerGluValArgAlaAlaArgLeuLeuLeuArgArgCysPro 584
 Db 1683 GGCGAGTGCCTATCGCAGCTGGGTAGGGCTGCCGCCCTCTCGCTCGCTGCTGCCG 1742
 Qy 585 LeuTrpGlyAspAlaThrCysLeuGlnLeuAlaMetGlnAlaAspAlaArgAlaPhePhe 604
 Db 1743 CTCTGGGGGAGATGCACTTCTGCTCCAGCTGGCCATGCAAGCTGACGCCGTGGCTTCTT 1802
 Qy 605 AlaGlnAspGlyValGlnSerLeuLeuThrGlnLysTrpTrpGlyAspMetAlaSerThr 624
 Db 1803 GCCCAGGATGGGTACAGTCTCTGCTGACACAGAGTTGGGGAGATATGCCAGCACT 1862
 Qy 625 ThrProIleTrpAlaLeuValLeuAlaPhePheCysProProLeuIleIyrThrArgLeu 644
 Db 1863 ACACCCATCTGGGCCCTGGTCTCCGCCTCTTGGCCCTCAACTCACTACACCCGCCCTC 1922
 Qy 645 IleThrPheArgIysSerGluGluGluProThrArgGluGluLeuGluPheAspMetAsp 664
 Db 1923 ATCACCTTCAGGAAATCGAAGAGGCCACACGGAGGAGCTAGAGTTGACATGGAT 1982
 Qy 665 SerValleLeuAsnGlyGluGlyProAlaGlyThrAlaAspProAlaGluIysThrProLeu 684
 Db 1983 ATGTCATTAAATGGGGAAAGGGCTCTGGGGACGGCGACGCCAGCGAGAGACGCCGCTG 2042
 Qy 685 GlyValProArgGlnSerGlyArgProGlyCysCysGlyGlyArgCysGlyGlyArgArg 704
 Db 2043 GGGGTCCCGCGCCAGTCGGGCCCTCGGGITGCTGCGGGGCCGCTGCGGGGGGCCCGG 2102
 Qy 705 CysLeuArgArgTrpPheHisPheTrpGlyAlaProValThrIlePheMetGlyAsnVal 724
 Db 2103 TGCTCTAGGCCGCTGGTCTCACTTCCTGGGGCGGCCGCGTGAACCATCTTCACTGGCAACGTC 2162
 Qy 725 ValSerTyrLeuLeuPheLeuLeuLeuPheSerArgValLeuLeuValAspPheGlnPro 744
 Db 2163 GTCAACCTACCTGCTGTTCTGCTGCTTCTCGCGGGTGCCTGCTGTTGAGTTCCAGCGG 2222
 Qy 745 AlaProGlySerLeuGluLeuLeuLeuIysPheTrpAlaPheThrLeuLeuCysGlu 764
 Db 2223 GGGCGGCCGCGCTCCCTGGAGCTGCTGCTATTTCTGGCTTACAGCTGCTGTGCGAG 2282
 Qy 765 GluLeuArgGlnGlyLeuSerGlyGlyGlyGlySerLeuAlaSerGlyGlyProGlyPro 784

Db	2283	GAACCTGGCCGAGGCCCCCTGAGCGGAGGCAGGGGAGCCTCGCCAGGGGGGCCCGGGGCT 2342
Qy	785	GlyHisAlaSerLeuSerGlnArgLeuArgLeuIleLeuAlaAspSerTrpAsnGlnCys 804
Db	2343	GCGCATGCCCTCACGAGCCAGGCCCCCTGCGGCCCTACCTCGGCCACAGCTGGAAACCACTGC 2402
Qy	805	AspLeuValAlaLeuIthrCysPheLeuLeuGlyValGlyCysArgLeuThrProGlyLeu 824
Db	2403	GACCTAGTGGCTCTCACCTGCTTCCCCTCTGGCGCTTGCGCTCGGCCCTGACCCGGTTTG 2462
Qy	825	TyrHisLeuGlyArgThrValLeuCysIleAspPheMetValPheThrValArgLeuLeu 844
Db	2463	TACCACTGGGCCGACTGTCTCTGATCGACTCTGATGGTTTACGGTGCGGCTGCTT 2522
Qy	845	HisAlaPheThrValAsnLysGlnLeuGlyProLysIleValIleValSerLysMetMet 864
Db	2523	CACATCTTCAACGCGAACAAACAGCTGGGGCCCAAAGATCCTCATGGTGAAGAAAGATGATG 2582
Qy	865	LysAspValPhePhePheLeuPhePheLeuGlyValTrpLeuValAlaTyrGlyValAla 884
Db	2583	AAGGACGTGTTCTCTCTCTCTCTCTGGCTGGCTGTGGCTGAGCTATGGCTGGCC 2642
Qy	885	ThrGluGlyLeuLeuArgProArgAspSerAspPheProSerIleLeuArgArgValPhe 904
Db	2643	ACGSGAGGGGCTCTGAGGCCAACGGGAGCTGACTTCCCAGTATOCCTGGGCCGCGCTTC 2702
Qy	905	TyrArgProTyrlLeuGlnIlePheGlyGlnIleProGlnGluAspMetAspValAlaLeu 924
Db	2703	TACCGTCCCCTACCTCGACATTCGCGCAAGATTCCCGAGGGACATGGACGTGGCCCTC 2762
Qy	925	MetGluHisSerAsnCysSerSerGluProGlyheTrpAlaHisProProGlyAlaGln 944
Db	2763	ATGGAGCACAGCGAACATGCTCTCGAGGCCGGCTCTGGCACACCCCTCTGGGGCCAG 2822
Qy	945	AlaGlyThrCysValSerGlnTyrAlaAsnTrpLeuValLeuLeuValIlePhe 964
Db	2823	GCGGGCACCTGGCTTCCAGATGCGCAACTGGCTGTGGTGCCTCCCTCGCTCATCTC 2882
Qy	965	LeuLeuValAlaAsnIleLeuLeuValAlaAsnLeuLeuIleAlaMetPheSerTyrThrPhe 984
Db	2883	CTGCTCTGGGCAAACATCTGCTGGTCAACTTGTCTATGCCATGTTCACTGACAACTTC 2942
Qy	985	GlyLysValGlnGlyAsnSerAspLeuTyrTrpLysAlaGlnArgTyrArgLeuIleArg 1004
Db	2943	GGCAAAGTACAGGGCACACGGCATCTACTGGAAAGGGCAGCGGTACCGCCTCATCGG 3002
Qy	1005	GluPheHisSerArgProAlaLeuAlaProProPheIleValIleSerHisLeuArgLeu 1024
Db	3003	GAATTCACACTCTGGCCGGCGCTGGGCCGGCCCTTTATCGCTCATCTCCACCTGGGCCCTC 3062
Qy	1025	LeuLeuArgGlnLeuCysArgArgProArgSerProGlnProSerSerProAlaLeuGlu 1044
Db	3063	CTGCTCAGGCAAATTGTGAGGGCACCCGGAGCCCCAGCGCTCTCCCGGCCCTCGAG 3122
Qy	1045	HisPheArgAlaTyrLeuSerLysGluAlaGluArgLysIleLeuLeuThrTrpGluSerVal 1064
Db	3123	CATCTCCGGGTTTACCTTCTAAAGGAAGCGAGCGGAAGCTGCTTAACGTGGGAATCGGTG 3162
Qy	1065	HisLysGluAsnPheLeuLeuAlaArgAlaArgAspLysArgGluSerAspSerGluArg 1084
Db	3183	CATAAGGAGAGATTCTGCTGGCACGGCTAGGGACAAGCGGGAGAGCGACTCCGGAGCGT 3242
Qy	1085	LeuGluArgThrSerGlnLysValAspLeuAlaLeuLysGlnLeuGlyHisIleArgGlu 1104
Db	3243	CTGGAGGGCACGTCGGAGGGTGGACTTGGCACTGAAACAGCTGGACACATCCCGAG 3302
Qy	1105	TyrGluGlnArgLeuLysValLeuGluArgGluValGlnGlnCysSerArgValLeuGly 1124
Db	3303	TACGAAACAGCGCTGAAAGTCTGGAGCGGGAGGGTCCAGCAGTGTAGCCGGCTCTGGGG 3362
Qy	1125	TrpValThr 1127
Db	3363	TGGGTGACG 3371

